



DECLARATION
Page 1 of 2

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Nadejda G. Gurskaya, et al.

Serial No.: 10/501,629

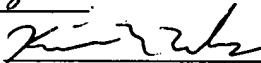
Confirmation No.: 9951

Filed: July 15, 2004

For: NOVEL FLUORESCENT
PROTEIN FROM AEQUOREA
COERULSCENS AND
METHODS FOR USING THE
SAME

§
§
§
§ Group Art Unit: 1656
§
§ Examiner: Maryam Monshipouri
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§
§
§
§
§
§
§

MAIL STOP AMENDMENT
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING 37 CFR 1.8	
I hereby certify that this correspondence is being deposited with sufficient postage as first class mail in an envelope addressed to: Mail Stop Amendment, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on <u>3/28/2008</u>	
Keith M. Tackett Typed Name 32,008 Reg. No. if applicable	 Signature (713) 623-4844 Telephone Number

DECLARATION UNDER 37 C.F.R. §1.132

I, Sergey Lukyanov, hereby declare and state that:

1. I am a scientist at Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry (Moscow, Russia), Evrogen JSC, and I am one of the inventors of the subject application.
2. I have worked in the molecular biology field for 22 years.
3. I have a Ph.D. degree in Molecular Biology from 1993 and a D.Sc. degree in Molecular Biology from 1999.
4. I declare that I have read the specification of United States Patent Application Serial No. 10/501,629 (the '629 application), filed July 15, 2004, the pending claims and the final Office Action dated January 23, 2008.

DECLARATION
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5. Paragraphs [00105] and [00106] of the '629 application describe a MegAlign algorithm used to determine "sequence identity."
6. The MegAlign clustal algorithm described in the '629 application is calculated by comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100. The MegAlign algorithm accounts for all mismatches, without preference, regardless of whether or not the mismatch is a conserved mismatch.
7. As used in the '629 application, common understanding of the term "sequence identity" also requires comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100.
8. Based on the description in the '629 application, the claim language "at least 96% identical" is understood to be determined by the following equation:
$$(\text{number of amino acid matches}) / (\text{total number of amino acids}) * 100.$$
9. Attachments 3 and 4 of the final Office Action identify a "Query Match" term and a "Best Local Similarity" term. The "Query Match" term does not consider conservative mismatches equivalent to other mismatches. As an example, Attachment 3 identifies "Length 238" and "Matches 221" such that $(\text{number of amino acid matches}) / (\text{total number of amino acids}) * 100$ is:
$$221 / 238 * 100 = 92.9\%$$
 (the same as the "Best Local Similarity").
10. Sequences shown in Attachments 3 and 4 of the final Office Action are respectively only 92.9% and 91.2% identical to SEQ ID NO: 2 referenced in claim 1 of the '629 application, and thereby are not "at least 96% identical to the *Aequorea coerulescens* non-fluorescent protein of SEQ ID NO: 2," as recited in claim 1.

The undersigned, Sergey Lukyanov, hereby declares that all statements made herein of my own knowledge are true and that these statements made on information and belief are believed to be true and further that these statements were made with knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of this application or any patent resulting therefrom.

Date: March, 27, 2008

Signature: 

MAR 3 1 2008

SEQUENCE LISTING

<110> Gurskaya, Nadejda
Fradkov, Arkadiy
Lukyanov, Sergey
Punkova, Natalia

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<140> US 10/501,629

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 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
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 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Thr Leu Ser
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 130 135 140
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 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
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Phe	Phe	Lys
Ser	Ala	Met
Pro	Glu	Gly
Gly	Tyr	Ile
Ile	Gln	Glu
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Gly	Asn	Tyr
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Arg	Ala	Glu
Val		
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Leu	Val	Asn
Arg	Ile	Glu
Leu	Thr	Gly
Thr		
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Gly	Asn	Ile
Ile	Leu	Gly
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Lys	Met	Glu
Glu	Tyr	Asn
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Ile	Glu	Asp
Gly	Ser	Val
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Asn	Thr	Pro
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Gly	Pro	
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Val	Leu	Leu
Pro	Asp	Asn
His	Tyr	Leu
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His	Met	Ile
Ile	Tyr	Phe
Glu	Phe	Val
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 <213> Aequoria coerulescens

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 gatgttaatg ggcacaaatt ctctgtcagt ggagagggcg aaggtgatgc gacatacgga 120
 aagttaaccc tttaaatttat ttgcactaca ggaaaactac ctgttccatg gccaacactt 180
 gtcactactc tctcttatgg tttcaatgc ttttcaagat atccagatca tatgaaacag 240
 catgacttct tcaagagtgc catgcctgaa gtttatatac aggaaagaac tatattttc 300
 gaagatgacg ggaactacaa gtcgcgtgcgtaa gaagtcaagt tcgagggtga tacccctgg 360
 aatagaatcg agttaacagg tactgatttt aaagaagatg gaaacatcct tgaaataaaa 420
 atgaaataca actataacgc acataatgta tacatcatga cagacaaagc aaaaaatgg 480
 atcaaagtta acttcaaaat tagacacacaac attgaagatg gaagcgttca acttgccagac 540
 cattatcaac aaaatactcc aattggcgat ggcctgtcc ttttaccaga taaccattac 600
 ctgtcccacac aatctgccct ttccaaagat cccaaacgaaa agagagatca catgatcctg 660
 tttgagtttg taacagctgc tgcgattaca catggcatgg atgaactata caaataa 717

<210> 16
 <211> 238
 <212> PRT
 <213> Aequoria coerulescens

<400> 16
 Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile
 1 5 10 15
 Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35	40	45
Thr	Thr	Gly
Lys	Leu	Pro
Pro	Val	Pro
Trp	Pro	Thr
Leu	Val	Thr
Thr	Thr	Leu
50	55	60
Ser	Tyr	Gly
Val	Gln	Cys
Phe	Ser	Arg
Tyr	Pro	Asp
His	Met	Lys
65	70	75
Asp	Asp	Gly
Phe	Phe	Tyr
Lys	Ser	Ile
Ala	Met	Gln
Pro	Glu	Glu
Gly	Tyr	Arg
85	90	95
Thr	Ile	Phe
Phe	Phe	Glu
Glu	Asp	Asp
Asp	Gly	Asn
Tyr	Lys	Ser
Lys	Arg	Ala
100	105	110
Lys	Phe	Glu
Glu	Gly	Asp
Asp	Thr	Leu
Leu	Val	Asn
Arg	Ile	Glu
115	120	125
Asp	Phe	Leu
Lys	Glu	Gly
Asn	Ile	Asn
130	135	140
Tyr	Asn	Ala
Ala	His	Asn
Asn	Val	Tyr
145	150	155
Ile	Met	Thr
Met	Asp	Lys
Asn	Ala	Lys
Gly	Asn	Gly
160		
Ile	Lys	Val
Val	Asn	Phe
Phe	Lys	Ile
Ile	Arg	His
His	Asn	Ile
Asn	Glu	Asp
165	170	175
Gly	Ser	Val
Gln	Leu	Ala
Ala	Asp	His
His	Tyr	Gln
Gln	Gln	Asn
Asn	Thr	Pro
180	185	190
Ile	Gly	Ile
Gly	Asp	Gly
Pro	Pro	Pro
195	200	205
Lys	Asp	Pro
Pro	Asn	Glu
Glu	Lys	Arg
Arg	Asp	His
His	Met	Ile
Met	Ile	Phe
Phe	Glu	Phe
Val	210	215
220		
Thr	Ala	Ala
Ala	Ile	Thr
Ile	His	Gly
His	Met	Asp
Met	Glu	Leu
Asp	Leu	Tyr
Tyr	Lys	
225	230	235

<210> 17
 <211> 717
 <212> DNA
 <213> Aequoria coerulescens

<400> 17
 atgagtaaag gaggcagaact tttcaactgga attgtcccaa ttcttatttgaa attaaatgg 60
 gatgttaatg ggcacaaatt ctctgtcagt ggagagggcg aaggtgatgc gacatacgga 120
 aagttaaccc tttaaatttat ttgcactaca ggaaaactac ctgttccatg gccaacactt 180
 gtcactactc tctcttatgg tttcaatgc ttttcaagat atccagatca tatgaaacag 240
 catgacttct tcaagagtgc catgcctgaa ggttatatac aggaaagaac tatattttc 300
 gaagatgacg ggaactacaa gtcgcgtgct gaagtcaagt tcaagggtga taccctgg 360
 aatagaatcg agttaacagg tactgatttt aaagaagatg gaaacatcct tgaaataaaa 420
 atgaaataca actataacgc acagaatgta tacatcatga cagacaaagc aaaaaatgg 480
 atcaaagtta acttcaaaat tagacacaaac attgaagatg gaagcgttca acttgcagac 540
 cattatcaac aaaatactcc aattggcgat ggcctgtcc ttttaccaga taaccattac 600
 ctgtcccacac aatctggccct ttccaaagat cccaaacgaaa agagagatca catgatcctg 660
 ctggagtttg taacagctgc tgcgattaca catggcatgg atgaactata ccaataa 717

<210> 18
 <211> 238
 <212> PRT
 <213> Aequoria coerulescens

<400> 18
 Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile
 1 5 10 15
 Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35	40	45	
Thr Thr Gly Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
50	55	60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg			
85	90	95	
Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val			
100	105	110	
Lys Phe Lys Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr			
115	120	125	
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn			
130	135	140	
Tyr Asn Ala Gln Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly			
145	150	155	160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
165	170	175	
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro			
180	185	190	
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser			
195	200	205	
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val			
210	215	220	
Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Gln			
225	230	235	

<210> 19
<211> 717
<212> DNA
<213> Aequoria coerulescens

<400> 19
atgagtaaag gagcagaact tttcaactgga attgtccaa ttcttattga attaaatgg 60
gatgttaatg ggcacaaatt ctctgtcagt ggagagggcg aaggtgatgc gacatacgga 120
aaggtaaccc ttaaatttat ttgcactaca ggaaaactac ctgttccatg gccaacactt 180
gtcgtactc tctcttatgg tttcaatgc tttcaagat atccagatca tatgaaacag 240
catgacttct tcaagagtgc catgcctgaa gtttatatac aggaaagaaac tatattttc 300
gaagatgacg ggaactacaa gtcgcgtgct gaagtcagt tcgagggtga taccctgg 360
agttagaatcg agttaacagg tactgattt aaagaagatg gaaacatcct tgaaataaa 420
atgaaataca actataacgc aactaatgta tacatcatga cagacaaagc aaaaaatgga 480
atcaaagtta acttcaaaat tagacacaac attaaagatg gaagcgttca acttgagac 540
cattatcaac aaaatactcc aattggcgat ggcctgtcc ttttaccaga taaccattac 600
ctgtcccacac aatctgccct ttccaaagat cccaaacgaaa agagagatca catgatctat 660
ttttagtttgc taacagctgc tgcgattaca catggcatgg atgaactata caaataa 717

<210> 20
<211> 238
<212> PRT
<213> Aequoria coerulescens

<400> 20
Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile
1 5 10 15
Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Ala Thr Leu		
50	55	60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg		
85	90	95
Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val		
100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Ser Arg Ile Glu Leu Thr Gly Thr		
115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn		
130	135	140
Tyr Asn Ala Thr Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Glu Phe Val		
210	215	220
Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 21
 <211> 717
 <212> DNA
 <213> Aequoria coerulescens

<400> 21
 atgagtaaag gagcagaact tttcaactgga attgtccaa ttcttattga attaaatgg 60
 gatgttaatg ggcacaaatt ctctgtcagt ggagagggcg aaggtgatgc gacatacgga 120
 aagttAACCC ttAAATTAT ttgcactaca ggAAAactac ctgttccatg gccaacactt 180
 gtcactactc tctcttatgg tttcaatgc ttttcaagat atccagatca tatgaaacag 240
 catgacttct tcaagagtgc catgcctgaa gtttatatac aggaaagaaac tatattttc 300
 gaagatgacg ggaactacaa gtcgcgtgct gaagtcaagt tcgagggtga tacccctgg 360
 aatagaatcg agttaacagg tactgattt aaagaagatg gaaacatcct tgaaataaaa 420
 atggaataaca actataacgc atctaatgta tacatcatga cagacaaagc aaaaaatgg 480
 atcaaagtta acttgaaaat tagacacaac attgcagatg gaagcgttca acttgcagac 540
 cattatcaac aaaatactcc aattggcgat ggcctgtcc ttttaccaga taaccattac 600
 ctgtcccacac aatctgccct ttccaaagat cccaaacgaaa agagagatca catgatctat 660
 tttgagtttgc taacagctgc tgcgattaca catggcatgg atgaactata caaataa 717

<210> 22
 <211> 238
 <212> PRT
 <213> Aequoria coerulescens

<400> 22
 Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile
 1 5 10 15
 Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50	55	60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg		
85	90	95
Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val		
100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr		
115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn		
130	135	140
Tyr Asn Ala Ser Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly		
145	150	155
Ile Lys Val Asn Leu Lys Ile Arg His Asn Ile Ala Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Glu Phe Val		
210	215	220
Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Ile Lys		
225	230	235

<210> 23

<211> 717

<212> DNA

<213> Aequoria coerulescens

<400> 23

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atgagcaagg gcgccgagct gttcacccgc atcgtgccc tcctgatcga gctgaatggc 60
gatgtaatg gccacaagtt cagcgtgagc ggcgagggcg agggcgatgc cacctacggc 120
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ctgtgccctg gcccaccctg 180
gtgaccaccc tgagctacgg cgtgcagtgc ttctcacgct accccgatca catgaagcag 240
cacgacttct tcaagagcgc catgccttag ggctacatcc aggagcgcac catcttcttc 300
gaggatgacg gcaactacaa gtcgcgcgc gaggttaagt tcgagggcga tacacctggtg 360
aatcgcatcg agctgaccgg caccgatttc aaggaggatg gcaacatcct gggcaataag 420
atggagtaca actacaacgc ccacaatgtg tacatcatga ccgacaaggc caagaatggc 480
atcaaggtga acttcaagat ccgccacacaac atcgaggatg gcagcgtgca gctggccgac 540
cactaccagc agaataacccc catcggcgt ggcctgtgc tgctgcccga taaccactac 600
ctgtccaccc agagcgcct gtccaaggac cccaaacgaga agcgcgatca catgatctac 660
ttcggcttcg tgaccggcgc cgccatcacc cacggcatgg atgagctgta caagtga 717

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<210> 24

<211> 238

<212> PRT

<213> Aequoria coerulescens

<400> 24

Met Ser Lys Gly Ala Glu Leu Phe Thr Gly Ile Val Pro Ile Leu Ile			
1	5	10	15
Glu Leu Asn Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20	25	30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			

35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50	55	60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Ile Gln Glu Arg		
85	90	95
Thr Ile Phe Phe Glu Asp Asp Gly Asn Tyr Lys Ser Arg Ala Glu Val		
100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Thr Gly Thr		
115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly Asn Lys Met Glu Tyr Asn		
130	135	140
Tyr Asn Ala His Asn Val Tyr Ile Met Thr Asp Lys Ala Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Tyr Phe Gly Phe Val		
210	215	220
Thr Ala Ala Ala Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 25
<211> 238
<212> PRT
<213> Aequoria coerulescens

<400> 25		
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1	5	10
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20	25	30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35	40	45
Thr Thr Gly Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50	55	60
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln		
65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85	90	95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
210 215 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225 230 235